WHAT IS CLAIMED IS:

1	1.	A met	thod for identifying a test composition or agent which modulates the
2		efficie	ncy of translation termination which comprises:
3		(a)	contacting the MTT1 with a test composition or agent under conditions
4			permitting binding between the MTT1 and the test composition;
5		(b)	detecting specific binding of the a test composition or agent to the MTT1;
6			and
7		(c) ·	determining whether the a test composition or agent inhibits the MTT1 so
8			as to identify a test composition or agent which is which modulates the
9			efficiency of translation termination.
1	2.	A meth	hod of identifying a test composition or agent which modulates binding to
2		MTT1,	, the method comprising:
3		(a)	incubating components comprising the test composition, and MTT1
4			wherein the incubating is carried out under conditions sufficient to permit
5			the components to interact; and
6		(b)	measuring the effect of the test composition on the binding to MTT1.
1	3.	The m	ethod of claim 2, further comprising identifying a gene comprising;
2		(a)	introducing into a cell a test composition which modulates
3	bin	ding to	MTT1;
4		(b)	determining the phenotype of the cell after (a);
5		(c)	comparing the cellular phenotype after (a) with the cellular phenotype
6			before (a); and
7		(d)	identifying the gene of the cell into which the test composition has been
8			introduced.

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- 4. A method of detecting a nonsense suppression disorder associated with the expression of mtt1 protein, wherein the method comprises contacting a sample from a subject having or suspected of having a disorder with a reagent that detects expression of the mtt1 protein and detecting the binding of the reagent in the sample.
- 5. An agent which inhibits, facilitates, or modulates the helicase, ATPase activity of MTT1.
- 1 6. The agent of claim 5, wherein the agent is a ribozyme, antisense molecule, or ligand which acts as an antagonist or agonist of translation termination.
- 7. An isolated multiprotein complex comprising a MTT1 gene, human Upf1p protein, a peptidyl eucaryotic release factor 1 (eRF1) and a peptidyl eucaryotic release factor 3 (eRF3), wherein the complex is effective to modulate peptidyl transferase activity during translation.
- 8. The complex of claim 7, further comprising human Upf3p and/or Upf2p.
- 9. An antibody which binds to the complex of claim 7.
- 1 10. The antibody of claim 9, wherein the antibody is a monoclonal or polyclonal
- 1 11. The antibody of claim 9, wherein the antibody has a label.
- 1 12. An agent which binds to the complex of claims 7 or 8.
- 1 13. An agent which inhibits or modulates the binding of human MTT1 to eRF3; or MTT1 ro a polysome.

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nonsense codon and/or

14. An agent which facilitates the binding of human MTT1 to eRF3; or MTT1 ro a 1 2 polysome. 15. The agent of claim 12, wherein the agent has a label or marker. 1 16. The agent of claim 14, wherein the agent is an antisense molecule or a ribozyme. 1 17. A method of modulating peptidyl transferase activity during translation, 1 comprising contacting a cell with the complex of claim 7 in an amount effective 2 to facilitate translation termination, thereby modulating the peptidyl transferase 3 activity. 4 18. A method of modulating peptidyl transferase activity during translation, 1 comprising contacting a cell with the agent of claim 12, in an amount effective 2 to suppress nonsense translation termination, thereby modulating the peptidyl 3 4 transferase activity. 19. The method of claim 18, wherein the peptidyl transferase activity during 1 translation comprises initiation, elongation, termination and degradation of 2 mRNA. 3 20. A method of modulating the efficiency of translation termination of mRNA at a 1

21. A method of screening for a drug involved in peptidyl transferase activity during translation comprising: a) contacting cells with a candidate drug; and b) assaying

codon and/or promoting degradation of abberant transcripts.

comprising contacting a cell with the agent of claim 12, in an amount effective

to modulate the efficiency of translation termination of mRNA at a nonsense

promoting degradation of abberant transcripts,

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- for modulation of the complex of claims 7, wherein a drug that modulates complex is involved in peptidyl transferase activity.
- 22. A method of screening for a drug active involved in enhancing translation termination comprising: a) contacting cells with a candidate drug; and b) assaying for modulation of the protein complex of claims 7; wherein a drug that modulates protein complex is involved in enhancing translation termination.
 - 23. A method of screening for a drug involved in enhancing translation termination comprising: a) incubating the drug and the complex; and b) measuring the effect on nonsense suppression, thereby screening for a drug involved in enhancing translation termination.
 - 24. The method of claim 23, wherein the assay is a RNA assay or a ATPase assay.
- 25. A method of screening for a drug which inhibits the interaction between MTT1 and eRF3, comprising: a) contacting cells with a candidate drug; and b) assaying for modulation of the complex of claim 7, wherein a drug that modulates the binding of MTT1 to eRF3 is involved in enhancing translation termination.
 - 26. A method of modulating the efficiency of translation termination of mRNA and/or degradation of abberant transcripts in a cell, said method comprising: a) providing a cell containing a vector comprising the nucleic acid encoding the complex of claim 7; or an antisense thereof; b) overexpressing said vector in said cell to produce an overexpressed complex so as to interfere with the function of the complex.
 - 27. A method for identifying a disease state involving a defect in the complex of claim 7 comprising: (a) transfecting a cell with a nucleic acid which encodes the complex; (b) determining the proportion of the defective complex of the cell after

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4	transfection; (c) comparing the proportion of the defective complex of the cell
5	after transfection with the proportion of defective complex of the cell before
6	transfection.
1	28. A method for treating a disease associated with peptidyl transferase activity,
2	comprising administering to a subject a therapeutically effective amount of a
3	pharmaceutical composition comprising the complex of claim 7 or the agent of
4	claim 12, and a pharmaceutical carrier or diluent, thereby treating the subject.
1	29. The method of claim 28, wherein the disease results from a nonsense or
2	frameshift mutation.
1	30. The method of claim 29, wherein the disease is β -thalassemia, β -globin,
2	Duchenne/Becker Muscular Dystrophy, Hemophilia A, Hemophilia B, Von
3	Willebrand Disease, Osteogenesis Imperfecta (OI), Breast cancer, Ovarian
4	Cancer, Wilms Tumor, Hirschsprung disease, Cystic fibrosis, Kidney Stones,
5	Familial hypercholesterolemia (FH), Retinitis Pigmentosa, or
6	Neurofibromatosis, Retinoblastoma, ATM, Costmann Disease.
•	31. A method for identifying a disease state involving defective multimeric proteins
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2	comprising:
3	(a) transfecting a cell with the vector of claim;
4	(b) determining the proportion of defective multimeric proteins of the cell
5	after tansfection;
6	(c) comparing the proportion of defective multimeric proteins of the cell after
7	transfection with the proportion of defective multimeric proteins of the
8	cell before transfection.

32. A method of identifying genes which are involved in modulation of translation

termination, which comprises: a) isolated a gene of interest; and b) determining

3	whether the gene of interest comprises motifs I-IX, wherein if the gene comprises
4	any one of the nine motifs the gene modulates translation fidelity including
5	iniatiatioin, elongation, termination, termination, decay.
1	33. The method of claim 32, wherein the motif I comprises the sequence:
2	GppGTKTxT-X(n).
1	34. The method of claim 32, wherein the motif II comprises the sequence
2	riLxcaSNxAvDxl-X(n).
1	35. The method of claim 32, wherein the motif III comprises the sequence
2	vviDExxQaxxxxxiPi- X(n).
1	36. The method of claim 32, wherein the motif IV comprises the sequence xxi1
2	aGDxxQLp- X(n).
1	37. The method of claim 32, wherein the motif V comprises the sequence lxx SLF
2	erv- X(n).
1	38. The method of claim 32, wherein the motif VI comprises the sequence
2	LxxQYRMhpxisefpxYxgxL- X(n).
1	39. The method of claim 32, wherein the motif VII comprises the sequence
2	IgvitPYxxQvxxl- X(n).
1	40. The method of claim 32, wherein the motif VIII comprises the sequence
2	vevxtVDxFQGreKdxIilSc VR- X(n).

- 1 41. The method of claim 32, wherein the motif IX comprises the sequence
- 2 iGFLxdxRRINValTRak.